L Number	Hits	Search Text	DB	Time stamp
1	92	long adj1 range adj1 (PCR or polymerase adj1 chain)	USPAT; US-PGPUB	2002/08/06 13:56
2	16	(long adj1 range adj1 (PCR or polymerase adj1 chain)) same (ligation or ligated or ligate)	USPAT; US-PGPUB	2002/08/06 13:56

=> file medline biosis caplus
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FILE 'MEDLINE' ENTERED AT 13:55:30 ON 06 AUG 2002

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=> s long (w) range (w) (PCR or polymerase(w)chain)
L1 384 LONG (W) RANGE (W) (PCR OR POLYMERASE(W) CHAIN)

=> s l1 and liga?
L2 20 L1 AND LIGA?

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 10 DUP REM L2 (10 DUPLICATES REMOVED)

=> d 1-10 ti

L3 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2002 ACS
TI High efficiency methods of constructing plasmid vectors for gene knockout in embryonic stem cells

L3 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2002 ACS
TI High efficient methods of creating DNA constructs for gene knockout in embryonic stem cells

L3 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2002 ACS
TI Haplotyping method for multiple distal nucleotide polymorphisms using **long-range PCR**

L3 ANSWER 4 OF 10 MEDLINE DUPLICATE 1
TI Molecular haplotyping of genomic DNA for multiple single-nucleotide polymorphisms located kilobases apart using **long-range polymerase chain** reaction and intramolecular **ligation**.

L3 ANSWER 5 OF 10 MEDLINE DUPLICATE 2
TI Characterisation of the human GFRalpha-3 locus and investigation of the gene in Hirschsprung disease.

L3 ANSWER 6 OF 10 MEDLINE DUPLICATE 3
TI Genomic organization, 5'flanking region and tissue-specific expression of mouse phosphofructokinase C gene.

L3 ANSWER 7 OF 10 MEDLINE DUPLICATE 4
TI Heterogeneity in the vanB gene cluster of genomically diverse clinical strains of vancomycin-resistant enterococci.

L3 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2002 ACS
TI Extender PCR: a method for the isolation of sequences regulating gene expression from genomic DNA

L3 ANSWER 9 OF 10 MEDLINE DUPLICATE 5

TI Strategy to sequence the 89 exons of the human LRP1 gene coding for the lipoprotein receptor related protein: identification of one expressed mutation among 48 polymorphisms.

L3 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 6
TI Complete structural characterisation of the human aryl hydrocarbon receptor gene.

=> d 3, 4 bib ab

L3 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2002 ACS
AN 2002:488130 CAPLUS
DN 137:58558
TI Haplotyping method for multiple distal nucleotide polymorphisms using **long-range PCR**
IN Evans, William Edward; McDonald, Oliver Gene
PA USA
SO U.S. Pat. Appl. Publ., 11 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002081598	A1	20020627	US 2001-829113	20010409

AB The invention relates to methods for detecting genetic polymorphisms in an organism, particularly to the detection of genetic polymorphisms that are due to multiple distal nucleotide polymorphisms within a gene. Methods are provided for detg. the haplotype structure of a gene, or other contiguous DNA segment, having two or more nucleotide polymorphisms that are sepd. by kilobases of DNA. The methods involve the use of PCR amplification and DNA **ligation** to bring the nucleotide polymorphisms on a particular allele of the gene into close proximity to facilitate the detn. of haplotype structure. The method is exemplified by genotyping human thiopurine S-methyltransferase (TPMT) gene for two SNPs (G460A and A719G) sepd. by approx. 8 kb. A **long-range PCR** reaction is performed by two PCR reactions. The first PCR uses a DNA sample contg. the TPMT gene and a first set of oligonucleotide primers designed for the amplification of the two SNPs and the region of the TPMT gene sepg. them. The resulting approx. 8.7 kb PCR product is then circularized via intramol. **ligation**, and is subjected to a second PCR amplification using a second pair of oligonucleotide primers lying adjacent to the circular DNA. The second PCR product is approx. 1.2 kb and comprises both SNPs sepd. by 695 nucleotides. The haplotype structure of the second PCR product can then be detd. by std. methods for SNPs that are sepd. by less than about 1 kilobase.

L3 ANSWER 4 OF 10 MEDLINE DUPLICATE 1
AN 2002139610 IN-PROCESS
DN 21864881 PubMed ID: 11875363
TI Molecular haplotyping of genomic DNA for multiple single-nucleotide polymorphisms located kilobases apart using **long-range polymerase chain** reaction and intramolecular **ligation**.
AU McDonald Oliver G; Krynetski Eugene Y; Evans William E
CS St Jude Children's Research Hospital, Memphis, TN, USA.
SO PHARMACOGENETICS, (2002 Mar) 12 (2) 93-9.
Journal code: 9211735. ISSN: 0960-314X.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)

LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20020305
Last Updated on STN: 20020305
AB Genetic polymorphisms are well-recognized causes of interindividual differences in disease risk and treatment response in humans. For genes containing multiple single-nucleotide polymorphisms (SNPs), haplotype structure is often the principal determinant of phenotypic consequences, and haplotype distribution represents the best approach for assessing patterns of linkage disequilibrium. To permit more widespread molecular determination of haplotypes, we developed a simple yet robust method to determine haplotype structure for multiple SNPs located up to 30 kb apart in genomic DNA using **long-range polymerase chain** reaction (LR-PCR) and intramolecular **ligation**. Complete concordance was shown between the new method and conventional approaches, such as family pedigree analysis or cloning and sequencing. The availability of a simple method to directly determine haplotype structure using genomic DNA, without family pedigree analysis, cloning or complex instrumentation, provides an important new tool for elucidating the genetic determinants of drug disposition and effects, disease risk, and molecular evolution.

=> s intramolecular (3a) ligation
L4 78 INTRAMOLECULAR (3A) LIGATION

=> s l4 and haplotyp?
L5 2 L4 AND HAPLOTYP?

=> d 1-2 ti

L5 ANSWER 1 OF 2 MEDLINE
TI Molecular **haplotyping** of genomic DNA for multiple single-nucleotide polymorphisms located kilobases apart using long-range polymerase chain reaction and **intramolecular ligation**.

L5 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Molecular **haplotyping** of genomic DNA for multiple single-nucleotide polymorphisms located kilobases apart using long-range polymerase chain reaction and **intramolecular ligation**.

=> d 1 bib ab

L5 ANSWER 1 OF 2 MEDLINE
AN 2002139610 IN-PROCESS
DN 21864881 PubMed ID: 11875363
TI Molecular **haplotyping** of genomic DNA for multiple single-nucleotide polymorphisms located kilobases apart using long-range polymerase chain reaction and **intramolecular ligation**.
AU McDonald Oliver G; Krynetski Eugene Y; Evans William E
CS St Jude Children's Research Hospital, Memphis, TN, USA.
SO PHARMACOGENETICS, (2002 Mar) 12 (2) 93-9.
Journal code: 9211735. ISSN: 0960-314X.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20020305
Last Updated on STN: 20020305
AB Genetic polymorphisms are well-recognized causes of interindividual differences in disease risk and treatment response in humans. For genes

containing multiple single-nucleotide polymorphisms (SNPs), **haplotype** structure is often the principal determinant of phenotypic consequences, and **haplotype** distribution represents the best approach for assessing patterns of linkage disequilibrium. To permit more widespread molecular determination of **haplotypes**, we developed a simple yet robust method to determine **haplotype** structure for multiple SNPs located up to 30 kb apart in genomic DNA using long-range polymerase chain reaction (LR-PCR) and **intramolecular ligation**. Complete concordance was shown between the new method and conventional approaches, such as family pedigree analysis or cloning and sequencing. The availability of a simple method to directly determine **haplotype** structure using genomic DNA, without family pedigree analysis, cloning or complex instrumentation, provides an important new tool for elucidating the genetic determinants of drug disposition and effects, disease risk, and molecular evolution.

=>
=> d 8-10 bib ab
2 ANSWERS ARE AVAILABLE. SPECIFIED ANSWER NUMBER EXCEEDS ANSWER SET SIZE
The answer numbers requested are not in the answer set.
ENTER ANSWER NUMBER OR RANGE (1):end

=> d his

(FILE 'HOME' ENTERED AT 13:55:24 ON 06 AUG 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:55:30 ON 06 AUG 2002
L1 384 S LONG (W) (W) (PCR OR POLYMERASE(W)CHAIN)
L2 20 S L1 AND LIGA?
L3 10 DUP REM L2 (10 DUPLICATES REMOVED)
L4 78 S INTRAMOLECULAR (3A) LIGATION
L5 2 S L4 AND HAPLOTYP?

=> d l3 8-10 bib ab

L3 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2002 ACS
AN 1999:368306 CAPLUS
DN 131:165837
TI Extender PCR: a method for the isolation of sequences regulating gene expression from genomic DNA
AU Anon.
CS USA
SO BioTechniques (1999), 26(5), 804-806
CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB A new polymerase chain reaction (PCR)-based method is described for "walking" into previously uncloned regions of genomic DNA that negates the need for synthesis of double-stranded vectorette linkers, blocked oligonucleotide adaptors, or genomic DNA library construction and screening. The method relies on both the **ligation** of a single-stranded oligonucleotide adaptor to restriction enzyme-digested genomic DNA and the blocking of nonspecific replication of the adaptor-complementary strand by incorporation of a dideoxynucleotide. It involves Taq DNA polymerase-catalyzed extension from internal gene-specific sites that generates the complementary strand of the **ligated** adaptor sequence, thus producing the primer annealing sites necessary for the amplification of the desired target sequences. Restriction enzymes generating 5' overhanging ends can be used with this technique. Extender PCR can be used to clone both upstream (5') and/or

downstream (3') regulatory regions using antisense or sense internal gene-specific primers, resp. If used in conjunction with **long-range PCR** protocols, this technique can rapidly amplify fragments of several kilobase pairs in length, negating the need to construct and screen genomic DNA libraries. It is particularly useful for the isolation of promoter regions from information contained within expressed sequence tag (EST) databases. This technique was used to isolate promoter sequences from three different opsin genes of mantis shrimp, Gonodactylus oerstedii, and the 5'-untranslated region and initiation codon of an opiate receptor-like gene from Lymnaea stagnalis.

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 9 OF 10 MEDLINE DUPLICATE 5
AN 1999000832 MEDLINE
DN 99000832 PubMed ID: 9782078
TI Strategy to sequence the 89 exons of the human LRP1 gene coding for the lipoprotein receptor related protein: identification of one expressed mutation among 48 polymorphisms.
CM Erratum in: Genomics 1999 May 15;58(1):111
AU Van Leuven F; Stas L; Thiry E; Nelissen B; Miyake Y
CS Experimental Genetics Group (EGG), Center for Human Genetics (CME), Flemish Institute for Biotechnology (VIB), Campus Gasthuisberg, Leuven, Belgium.. fredvl@med.kuleuven.ac.be/legtegg/
SO GENOMICS, (1998 Sep 1) 52 (2) 138-44.
Journal code: 8800135. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF058397; GENBANK-AF058398; GENBANK-AF058399; GENBANK-AF058400; GENBANK-AF058401; GENBANK-AF058402; GENBANK-AF058403; GENBANK-AF058404; GENBANK-AF058405; GENBANK-AF058406; GENBANK-AF058407; GENBANK-AF058408; GENBANK-AF058409; GENBANK-AF058410; GENBANK-AF058411; GENBANK-AF058412; GENBANK-AF058413; GENBANK-AF058414; GENBANK-AF058415; GENBANK-AF058416; GENBANK-AF058417; GENBANK-AF058418; GENBANK-AF058419; GENBANK-AF058420; GENBANK-AF058421; GENBANK-AF058422; GENBANK-AF058423; GENBANK-AF058424; GENBANK-AF058425; GENBANK-AF058426; +
EM 199812
ED Entered STN: 19990115
Last Updated on STN: 20000303
Entered Medline: 19981207
AB The human lipoprotein receptor related protein (LRP) binds and internalizes a diverse set of **ligands**, making LRP the most multifunctional endocytic receptor known. This is possible due to the large size, i.e., 600 kDa, of the receptor protein containing three clusters of putative **ligand** binding domains, each structurally comparable to the classical LDL receptor. Based on previous structural analysis of the human LRP1 gene (Van Leuven et al., 1994, Genomics, 24: 78-89), a strategy was developed to sequence the 89 exons of the LRP1 gene, including partial intron sequences. The gene was amplified from individual genomic DNA by **long-range PCR**, in 14 amplicons sized between 0.4 and 11 kb that were used as templates for 110 sequencing primers. In total, 48 mutations and intronic polymorphisms were identified. Two previously reported polymorphisms, i.e., in the promoter region and in exon 3, were precisely defined by sequencing. The first expressed mutation, i.e., an alanine to valine transition at position 217 of the LRP precursor protein, was detected on one allele in 2 of 33 individuals. Although the strategy is still subject to refinement, this approach is reported to allow others to analyze genetic differences in the human LRP1 gene, with particular reference to the recently reported association with late-onset Alzheimer disease.

L3 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 6
AN 1996:155321 BIOSIS
DN PREV199698727456
TI Complete structural characterisation of the human aryl hydrocarbon receptor gene.
AU Bennett, P. (1); Ramsden, D. B.; Williams, A. C.
CS (1) University Department Medicine, Queen Elizabeth Hospital, Birmingham B15 2TH UK
SO Clinical Molecular Pathology, (1996) Vol. 49, No. 1, pp. M12-M16. ISSN: 1355-2910.
DT Article
LA English
AB Aims: To clone and characterise the complete structural gene for the human aryl hydrocarbon receptor (AhR). This gene, located on chromosome 7, encodes a cytosolic receptor protein which, upon activation by various xenobiotic **ligands**, translocates to the nucleus, where it acts as a specific transcription factor. Methods-Primers, based on the AhR cDNA sequence, were used in conjunction with recently developed **long range PCR** techniques to amplify contiguous sections of the cognate gene. The amplicons produced were then cloned and characterised. A cDNA probe was also used to screen a human P1 library. Results: Using the cDNA primers, DNA fragments which mapped the entire coding region of the gene were amplified and cloned. All but one of these fragments were amplified directly from human genomic DNA. The remaining fragment was amplified using DNA prepared from a P1 clone as the PCR template. This P1 clone, obtained by screening a human P1 library, also contained the entire Ab locus. Characterisation of amplified and cloned DNA fragments provided sufficient information for the construction of a complete structural map of the gene. This also included 150 base pairs of nucleotide sequence data at all intronic termini. Conclusions: These data indicate that the human AhR gene is about 50 kilobases long and contains 11 exons. The overall intron/exon structure of the human gene is homologous to that of the previously characterised mouse gene; however, it is probably some 20 kilobases larger. These results demonstrate the need for further characterisation and provide the data to facilitate this.

=> dup rem l4
PROCESSING COMPLETED FOR L4
L6 42 DUP REM L4 (36 DUPLICATES REMOVED)

=> d 1-42 ti

L6 ANSWER 1 OF 42 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Nucleosome linker proteins HMGB1 and histone H1 differentially enhance DNA ligation reactions.

L6 ANSWER 2 OF 42 MEDLINE DUPLICATE 1
TI Molecular haplotyping of genomic DNA for multiple single-nucleotide polymorphisms located kilobases apart using long-range polymerase chain reaction and **intramolecular ligation**.

L6 ANSWER 3 OF 42 MEDLINE DUPLICATE 2
TI pH-dependent modulation of relaxivity and luminescence in macrocyclic gadolinium and europium complexes based on reversible **intramolecular** sulfonamide **ligation**.

L6 ANSWER 4 OF 42 MEDLINE
TI A thioester ligation approach to amphipathic bicyclic peptide library.

L6 ANSWER 5 OF 42 MEDLINE DUPLICATE 3
TI Interactions of the DNA ligase IV-XRCC4 complex with DNA ends and the DNA-dependent protein kinase.

L6 ANSWER 6 OF 42 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 4
TI Peptide segment coupling by prior **ligation** and proximity-induced **intramolecular** acyl transfer.

L6 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2002 ACS
TI Catalytic Ring-Closing Metathesis of Doubly Armed, Bridged Bicyclic Sulfones. Evaluation of Chain Length and Possible **Intramolecular** SO2 Group **Ligation** to the Ruthenium Carbenoid

L6 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2002 ACS
TI **Intramolecular** orthogonal **ligation** for the synthesis of cyclic peptides

L6 ANSWER 9 OF 42 MEDLINE DUPLICATE 5
TI An apyrimidinic site kinks DNA and triggers incision by endonuclease VII of phage T4.

L6 ANSWER 10 OF 42 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Chemical ligation of unprotected peptides directly from a solid support.

L6 ANSWER 11 OF 42 MEDLINE DUPLICATE 6
TI Peach latent mosaic viroid is locked by a 2',5'-phosphodiester bond produced by in vitro self-ligation.

L6 ANSWER 12 OF 42 MEDLINE DUPLICATE 7
TI Molecular analysis of the cos region of the Lactobacillus casei bacteriophage A2. Gene product 3, gp3, specifically binds to its downstream cos region.

L6 ANSWER 13 OF 42 MEDLINE DUPLICATE 8
TI Cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.

L6 ANSWER 14 OF 42 MEDLINE DUPLICATE 9
TI Fos and Jun bend the AP-1 site: effects of probe geometry on the detection of protein-induced DNA bending.

L6 ANSWER 15 OF 42 MEDLINE DUPLICATE 10
TI Intracellular cleavage and ligation of hepatitis delta virus genomic RNA: regulation of ribozyme activity by cis-acting sequences and host factors.

L6 ANSWER 16 OF 42 MEDLINE DUPLICATE 11
TI Activities and substrate specificity of the evolutionarily conserved central domain of retroviral integrase.

L6 ANSWER 17 OF 42 CAPLUS COPYRIGHT 2002 ACS
TI **Intramolecular ligation** of carbonyl oxygen to central zinc in synthetic oligopeptide-linked zinc-porphyrins

L6 ANSWER 18 OF 42 MEDLINE DUPLICATE 12
TI Characterization of intra- and intermolecular DNA ligation mediated by eukaryotic topoisomerase I. Role of bipartite DNA interaction in the ligation process.

L6 ANSWER 19 OF 42 MEDLINE DUPLICATE 13
TI Site-directed mutagenesis of double-stranded DNA by the polymerase chain

reaction.

L6 ANSWER 20 OF 42 MEDLINE DUPLICATE 14
TI **Intramolecular** and intermolecular DNA **ligation** mediated by topoisomerase II.

L6 ANSWER 21 OF 42 MEDLINE DUPLICATE 15
TI Intermolecular ligation mediates efficient cotransformation in Phytophthora infestans.

L6 ANSWER 22 OF 42 MEDLINE DUPLICATE 16
TI Nonenymatic ligation of double-helical DNA by alternate-strand triple helix formation.

L6 ANSWER 23 OF 42 MEDLINE DUPLICATE 17
TI Ribonuclease T1 generates circular RNA molecules from viroid-specific RNA transcripts by cleavage and **intramolecular ligation.**

L6 ANSWER 24 OF 42 MEDLINE DUPLICATE 18
TI HMG 14 and protamine enhance ligation of linear DNA to form linear multimers: phosphorylation of HMG 14 at Ser 20 specifically inhibits intermolecular DNA ligation.

L6 ANSWER 25 OF 42 MEDLINE DUPLICATE 19
TI An integrative vector exploiting the transposition properties of Tn1545 for insertional mutagenesis and cloning of genes from gram-positive bacteria.

L6 ANSWER 26 OF 42 MEDLINE DUPLICATE 20
TI Two bases are deleted from the termini of HIV-1 linear DNA during integrative recombination.

L6 ANSWER 27 OF 42 MEDLINE DUPLICATE 21
TI Construction of a series of pSAM2-based integrative vectors for use in actinomycetes.

L6 ANSWER 28 OF 42 MEDLINE DUPLICATE 22
TI A novel DNA deletion-ligation reaction catalyzed in vitro by a developmentally controlled activity from Tetrahymena cells.

L6 ANSWER 29 OF 42 MEDLINE DUPLICATE 23
TI A 5' exo-ribonuclease and RNA ligase of T. brucei.

L6 ANSWER 30 OF 42 MEDLINE DUPLICATE 24
TI Effect of histone H1, poly(ethyleneglycol) and DNA concentration on intermolecular and **intramolecular ligation** by T4 DNA ligase.

L6 ANSWER 31 OF 42 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 25
TI BOTH-FACES HINDERED PORPHYRINS PART 4. SYNTHESIS OF FUNCTIONALIZED BASKET-HANDLE PORPHYRINS DESIGNED FOR A STRICT **INTRAMOLECULAR** AXIAL **LIGATION** IN SUPERSTRUCTURED COMPLEXES.

L6 ANSWER 32 OF 42 MEDLINE DUPLICATE 26
TI Mechanism and requirements of in vitro RNA splicing of the primary transcript from the T4 bacteriophage thymidylate synthase gene.

L6 ANSWER 33 OF 42 MEDLINE DUPLICATE 27
TI Regulation of inter- and **intramolecular ligation** with T4 DNA ligase in the presence of polyethylene glycol.

L6 ANSWER 34 OF 42 MEDLINE DUPLICATE 28
TI Variations of **intramolecular ligation** rates allow the detection of protein-induced bends in DNA.

L6 ANSWER 35 OF 42 MEDLINE DUPLICATE 29
TI Thermophilic HB8 DNA ligase: effects of polyethylene glycols and polyamines on blunt-end ligation of DNA.

L6 ANSWER 36 OF 42 MEDLINE
TI Influence of monovalent cations on the activity of T4 DNA ligase in the presence of polyethylene glycol.

L6 ANSWER 37 OF 42 MEDLINE
TI Hexamine cobalt chloride promotes intermolecular ligation of blunt end DNA fragments by T4 DNA ligase.

L6 ANSWER 38 OF 42 MEDLINE
TI A novel strategy for constructing clustered point mutations.

L6 ANSWER 39 OF 42 MEDLINE DUPLICATE 30
TI Oriented synthesis and cloning of influenza virus nucleoprotein cDNA that leads to its expression in mammalian cells.

L6 ANSWER 40 OF 42 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI ORIENTED SPECIFIC CLONING OF INFLUENZA VIRUS COMPLEMENTARY DNA LEADING TO THE EXPRESSION OF THE VIRAL GENES IN MAMMALIAN CELLS.

L6 ANSWER 41 OF 42 MEDLINE DUPLICATE 31
TI Expression of cloned hepatitis B virus DNA in human cell cultures.

L6 ANSWER 42 OF 42 MEDLINE DUPLICATE 32
TI Two adenovirus mRNAs have a common 5' terminal leader sequence encoded at least 10 kb upstream from their main coding regions.

=> d 38 bib ab

L6 ANSWER 38 OF 42 MEDLINE
AN 85215504 MEDLINE
DN 85215504 PubMed ID: 2987803
TI A novel strategy for constructing clustered point mutations.
AU Haltiner M; Kempe T; Tjian R
SO NUCLEIC ACIDS RESEARCH, (1985 Feb 11) 13 (3) 1015-25.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Dental Journals; Priority Journals
EM 198507
ED Entered STN: 19900320
Last Updated on STN: 19990129
Entered Medline: 19850718
AB We have modified the synthetic linker mutagenesis procedure (1,2) in order to facilitate both the construction and the analysis of deletions, insertions and clustered point mutations generated in DNA in vitro. The protocol as originally described by McKnight and Kingsbury (1) involved attaching a synthetic linker sequence to each 5' or 3' deletion endpoint in DNA. We have designed specific plasmid vectors that can be used to generate nested sets of deletion mutations in the DNA being analyzed. The utility of these vectors is that a linker sequence of choice can be inserted at the endpoint of a deletion in a single **intramolecular ligation** without the use of synthetic linker DNA. In a second

modification of the original procedure, we have adopted a rapid method for sequencing supercoiled plasmid DNAs from 10 ml cultures by primer extension. The site-directed mutagenesis strategy outlined here is suited for studying regulatory regions of DNA, such as origins of DNA replication, transcriptional promoters, enhancer elements, and activator binding sites. We have used this rapid and efficient strategy to generate deletions, insertions, and clustered point mutations in the transcriptional control region of a gene encoding the major human ribosomal RNAs.

=> s (PCR or polymerase(w)chain) (11w) (ligat? (4a) (amplified or product))
L7 115 (PCR OR POLYMERASE(W) CHAIN) (11W) (LIGAT? (4A) (AMPLIFIED OR PRODUCT))

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8 78 DUP REM L7 (37 DUPLICATES REMOVED)

=> d 1-78 ti

L8 ANSWER 1 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI A positive selection vector system for direct PCR cloning

L8 ANSWER 2 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI A positive selection vector system, pRGR, for direct cloning of PCR amplified DNA fragments based on reconstruction of a reporter gene or a regulatory gene

L8 ANSWER 3 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI High efficient methods of creating DNA constructs for gene knockout in embryonic stem cells

L8 ANSWER 4 OF 78 MEDLINE DUPLICATE 1
TI Cloning of Xanthomonas campestris pv. campestris pathogenicity-related gene sequences by TAIL-PCR.

L8 ANSWER 5 OF 78 MEDLINE DUPLICATE 2
TI Blockerette-ligated capture t7-amplified rt-PCR, a new method for determining flanking sequences.

L8 ANSWER 6 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Multiplex DNA amplification using ligase chain reaction and amplification of ligation products using families of ligatabale probes

L8 ANSWER 7 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Transmembrane one swapping between the human alpha2A-adrenergic receptor and its paralogues.

L8 ANSWER 8 OF 78 MEDLINE DUPLICATE 3
TI Cryoprotective effect of the serine-rich repetitive sequence in silk protein sericin.

L8 ANSWER 9 OF 78 MEDLINE DUPLICATE 4
TI Assignment of D-amino-acid oxidase gene to a human and a mouse chromosome.

L8 ANSWER 10 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Cj0634, a dprA homolog, is involved in DNA transformation of Campylobacter jejuni.

L8 ANSWER 11 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Cloning and expression of alkaline phosphatase gene from

Schizosaccharomyces pombe.

L8 ANSWER 12 OF 78 MEDLINE
TI cDNA cloning and sequence analysis of the lectin genes of the Korean mistletoe (Viscum album coloratum).

L8 ANSWER 13 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Construction of the full-length cDNA of dengue type 2 virus isolated in China.

L8 ANSWER 14 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Control of Lucina pectinata hemoglobin I redox properties through site-directed mutagenesis: cDNA library characterization.

L8 ANSWER 15 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Ligation-mediated PCR for quantitative in vivo footprinting

L8 ANSWER 16 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI A novel tumor blood vessel specific Fab antibody fragment: gene cloning, expression and activity

L8 ANSWER 17 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Cloning and sequencing of verotoxin 2 (VT2) gene from Escherichia coli O157:H7

L8 ANSWER 18 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Kinetics and specificity of cloned and expressed rat kidney mitochondrial dicarboxylate carrier exhibiting glutathione transport.

L8 ANSWER 19 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Cloning, sequencing and structural analysis of the protein kinase gene of a wild Chinese pseudorabies virus strain

L8 ANSWER 20 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Adaptation of inverse PCR to generate an internal deletion

L8 ANSWER 21 OF 78 MEDLINE DUPLICATE 5
TI Directional cloning of native PCR products with preformed sticky ends (autosticky PCR).

L8 ANSWER 22 OF 78 MEDLINE DUPLICATE 6
TI Preparation of recombinant human monoclonal antibody Fab fragments specific for Entamoeba histolytica.

L8 ANSWER 23 OF 78 MEDLINE DUPLICATE 7
TI Expression of beta-defensin genes by human salivary glands.

L8 ANSWER 24 OF 78 MEDLINE DUPLICATE 8
TI Quantitation of Toxoplasma gondii DNA in a competitive nested polymerase chain reaction.

L8 ANSWER 25 OF 78 MEDLINE
TI [Microcloning and characteristics of DNA from regions of the centromeric heterochromatin of Drosophila melanogaster polytene chromosomes]. Mikroklonirovanie i kharakteristika DNK iz raionov pritsentromernogo geterokhromatina politennykh khromosom Drosophila melanogaster.

L8 ANSWER 26 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Microcloning and characterization of DNA from pericentromeric heterochromatin of Drosophila melanogaster polytene chromosomes

L8 ANSWER 27 OF 78 MEDLINE DUPLICATE 9

TI The effect of 17beta-estradiol-DNA adducts on the replication of exon # 5 of the human suppressor gene p53.

L8 ANSWER 28 OF 78 MEDLINE DUPLICATE 10
TI PCR- and ligation-mediated synthesis of marker cassettes with long flanking homology regions for gene disruption in Saccharomyces cerevisiae.

L8 ANSWER 29 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Directional cloning of native PCR products with preformed sticky ends (autosticky PCR*)

L8 ANSWER 30 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Expression and purification of human plasminogen activator inhibitor type-2 in Escherichia coli

L8 ANSWER 31 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Cloning and sequencing of cDNA of the major protective antigen gene of a pathogenic swine vesicular disease virus strain

L8 ANSWER 32 OF 78 MEDLINE DUPLICATE 11
TI Amplification of target-specific, ligation-dependent circular probe.

L8 ANSWER 33 OF 78 MEDLINE DUPLICATE 12
TI Making genes green: creating green fluorescent protein (GFP) fusions with blunt-end PCR products.

L8 ANSWER 34 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Making genes green: creating green fluorescent protein (GFP) fusions with blunt-end PCR products

L8 ANSWER 35 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Cloning and sequencing of cDNA of the avian infectious bronchitis virus immunogen gene

L8 ANSWER 36 OF 78 MEDLINE DUPLICATE 13
TI Cloning of minisatellite-containing sequences from two-dimensional DNA fingerprinting gels reveals the identity of genomic alterations in low-grade gliomas of different patients.

L8 ANSWER 37 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI PCR-amplified cDNA probes for verification of differentially expressed genes

L8 ANSWER 38 OF 78 MEDLINE DUPLICATE 14
TI AFLP markers for DNA fingerprinting in cattle.

L8 ANSWER 39 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI AFLP markers for DNA fingerprinting in cattle.

L8 ANSWER 40 OF 78 MEDLINE DUPLICATE 15
TI Use of a PCR method based on IS6110 polymorphism for typing Mycobacterium tuberculosis strains from BACTEC cultures.

L8 ANSWER 41 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Shotgun antisense mutagenesis

L8 ANSWER 42 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI GC-rich template amplification by inverse PCR DNA polymerase and solvent effects

L8 ANSWER 43 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Optimized conditions for cloning PCR products into an XcmI T-vector

L8 ANSWER 44 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI A nucleic acid amplification procedure using a combination of elements from ligase and polymerase chain reactions

L8 ANSWER 45 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Japanese pear fruit dimple disease caused by apple scar skin viroid (ASSVd.

L8 ANSWER 46 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Expression profiling of mRNA obtained from single identified crustacean motor neurons: Determination of specificity of hybridization

L8 ANSWER 47 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Molecular cloning of kappa variable domain against human D-dimer

L8 ANSWER 48 OF 78 MEDLINE
TI The absence of ongoing immunoglobulin gene hypermutation suggests a distinct mechanism for c-myc mutation in endemic Burkitt's lymphoma.

L8 ANSWER 49 OF 78 MEDLINE DUPLICATE 16
TI Tertiary structure of an amyloid immunoglobulin light chain protein: a proposed model for amyloid fibril formation.

L8 ANSWER 50 OF 78 MEDLINE DUPLICATE 17
TI Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta.

L8 ANSWER 51 OF 78 MEDLINE DUPLICATE 18
TI Molecular cloning and expression of DNA encoding ovine interleukin 2.

L8 ANSWER 52 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Solid-phase nested deletion: a new subcloning-less method for generating nested deletions

L8 ANSWER 53 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 19
TI Molecular cloning and sequences of the HCV NS1 genomic region.

L8 ANSWER 54 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Cloning and expression of Escherichia coli ornithine transcarbamylase gene, argI.

L8 ANSWER 55 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI A novel method for the preparation of a cDNA for use in the analysis of the RNA using a DNA/RNA ligation product

L8 ANSWER 56 OF 78 MEDLINE
TI DNA analysis of cytochrome b positive chronic granulomatous disease (a case report).

L8 ANSWER 57 OF 78 MEDLINE DUPLICATE 20
TI T-cassette ligation: a method for direct sequencing and cloning of PCR-amplified DNA fragments.

L8 ANSWER 58 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Construction of the expression clone of an epitope gene of human cytomegalovirus by polymerase chain reaction.

L8 ANSWER 59 OF 78 MEDLINE DUPLICATE 21
TI Direct cloning of unmodified PCR products by exploiting an engineered

restriction site.

L8 ANSWER 60 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Tripartite fusion proteins of glutathione S-transferase (GST)

L8 ANSWER 61 OF 78 MEDLINE DUPLICATE 22
TI In vivo cloning of PCR products in E. coli.

L8 ANSWER 62 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Directional cloning of **PCR product** into plasmid by **ligation** independent cloning (LIC) method.

L8 ANSWER 63 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Efficient cloning of fragments of the polymerase chain reaction directly into the single stranded bacteriophage M13mp18

L8 ANSWER 64 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Single specific primer-polymerase chain reaction (SSP-PCR) and genome walking

L8 ANSWER 65 OF 78 MEDLINE
TI Generation of cohesive ends on PCR products by UDG-mediated excision of dU, and application for cloning into restriction digest-linearized vectors.

L8 ANSWER 66 OF 78 MEDLINE DUPLICATE 23
TI PCR MIMICS: competitive DNA fragments for use as internal standards in quantitative PCR.

L8 ANSWER 67 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Structural analysis of satellite RNA of arabis mosaic virus and its ribozyme.

L8 ANSWER 68 OF 78 MEDLINE DUPLICATE 24
TI A simple and fast method for cloning and analyzing polymerase chain reaction products.

L8 ANSWER 69 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Direct ligation of PCR products for cloning and sequencing

L8 ANSWER 70 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Extension product capture improves genomic sequencing and DNase I footprinting by ligation-mediated PCR

L8 ANSWER 71 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI DNA sequencing

L8 ANSWER 72 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI An efficient method for blunt-end ligation of PCR products

L8 ANSWER 73 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI A simple and rapid method for generating a deletion by PCR

L8 ANSWER 74 OF 78 MEDLINE DUPLICATE 25
TI A rapid isolation of the unknown 5'-flanking sequence of human CENP-B cDNA with polymerase chain reactions.

L8 ANSWER 75 OF 78 MEDLINE DUPLICATE 26
TI Construction of representative immunoglobulin variable region cDNA libraries from human peripheral blood lymphocytes without in vitro stimulation.

L8 ANSWER 76 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Screening of cDNA-libraries and gene reconstruction by PCR

L8 ANSWER 77 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Method for tapping the immunological repertoire

L8 ANSWER 78 OF 78 CAPLUS COPYRIGHT 2002 ACS
TI Method for constructing genes encoding heterodimeric receptors having a preselected specificity

=> d 74 bib ab

L8 ANSWER 74 OF 78 MEDLINE DUPLICATE 25
AN 92134737 MEDLINE
DN 92134737 PubMed ID: 1368745
TI A rapid isolation of the unknown 5'-flanking sequence of human CENP-B cDNA with polymerase chain reactions.
AU Sugimoto K; Himeno M
CS Department of Agricultural Chemistry, College of Agriculture, University of Osaka Prefecture, Japan.
SO AGRICULTURAL AND BIOLOGICAL CHEMISTRY, (1991 Nov) 55 (11) 2687-92.
Journal code: 0370452. ISSN: 0002-1369.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Biotechnology
EM 199203
ED Entered STN: 19950809
Last Updated on STN: 19950809
Entered Medline: 19920310
AB We rapidly and efficiently isolated the 5'-region of cDNA encoding the N-terminal region of human centromere antigen B (CENP-B) including an ATG methionine codon by **polymerase chain** reactions (**PCR**). The unknown 5'-flanking sequence of the cDNA was **amplified** using an adaptor-sequence **ligated** to the 5' end as a universal primer sequence. To locate the target fragments, we did an additional PCR with another set of two internal primers using samples of the size-fractionated products as templates, rather than using the conventional hybridization procedure. This approach can further be applied to the analysis of other unknown flanking sequences of cDNA or genomic DNA.

=> d his

(FILE 'HOME' ENTERED AT 13:55:24 ON 06 AUG 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:55:30 ON 06 AUG 2002
L1 384 S LONG (W) (W) (PCR OR POLYMERASE(W)CHAIN)
L2 20 S L1 AND LIGA?
L3 10 DUP REM L2 (10 DUPLICATES REMOVED)
L4 78 S INTRAMOLECULAR (3A) LIGATION
L5 2 S L4 AND HAPLOTYP?
L6 42 DUP REM L4 (36 DUPLICATES REMOVED)
L7 115 S (PCR OR POLYMERASE(W)CHAIN) (11W) (LIGAT? (4A) (AMPLIFIED OR
L8 78 DUP REM L7 (37 DUPLICATES REMOVED)

=> s (PCR or polymerase(w)chain) (11w) (ligat? (4a) (amplified or product)) (15w) reamplif?
L9 0 (PCR OR POLYMERASE(W) CHAIN) (11W) (LIGAT? (4A) (AMPLIFIED OR PRODUCT)) (15W) REAMPLIF?

=> s (PCR or polymerase(w)chain) (11w) (ligat?) (15w) reamplif?
L10 2 (PCR OR POLYMERASE(W) CHAIN) (11W) (LIGAT?) (15W) REAMPLIF?

=> d 1-2 ti

L10 ANSWER 1 OF 2 MEDLINE
TI Efficient reamplification of differential display products by transient ligation and thermal asymmetric PCR.

L10 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Efficient reamplification of differential display products by transient ligation and thermal asymmetric PCR.

=> d 1 bib ab

L10 ANSWER 1 OF 2 MEDLINE
AN 1998128019 MEDLINE
DN 98128019 PubMed ID: 9461480
TI Efficient reamplification of differential display products by transient ligation and thermal asymmetric PCR.
AU Bonnet S; Prevot G; Bourgouin C
CS Unite d'Ecologie des Systemes Vectoriels, Institut Pasteur, 25 rue du Docteur Roux, 75015 Paris, France.
SO NUCLEIC ACIDS RESEARCH, (1998 Feb 15) 26 (4) 1130-1.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199803
ED Entered STN: 19980326
Last Updated on STN: 19980326
Entered Medline: 19980317
AB A new method for specific reamplification of DDRT-**PCR** products is presented. After transient **ligation** of the primary DDRT-PCR fragments into a T-vector, the cDNAs of interest were **reamplified** by hemi-nested PCR and thermally asymmetric cycles. In contrast to the originally described protocol, this method of reamplification is specific, sensitive, reproducibly gives a high yield of DNA and allows direct sequencing of the reamplified product without purification or cloning.

=> s (PCR or polymerase(w)chain) (11w) (ligat?) (15w) amplif?
L11 104 (PCR OR POLYMERASE(W) CHAIN) (11W) (LIGAT?) (15W) AMPLIF?

=> dup rem l11
PROCESSING COMPLETED FOR L11
L12 80 DUP REM L11 (24 DUPLICATES REMOVED)

=> d 32 bib ab

L12 ANSWER 32 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1998:767292 CAPLUS
DN 130:163631
TI Subtracted, unique-sequence, in situ hybridization: Experimental and diagnostic applications
AU Davison, Jon M.; Morgan, Thomas W.; Hsi, Bae-Li; Xiao, Sheng; Fletcher, Jonathan A.
CS Brigham and Women's Hospital and Harvard Medical School, Departments of Pathology, Boston, MA, USA

SO American Journal of Pathology (1998), 153(5), 1401-1409
CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal
LA English
AB Nonrandom chromosomal aberrations, particularly in cancer, identify pathogenic biol. pathways and, in some cases, have clin. relevance as diagnostic or prognostic markers. Fluorescence and colorimetric in situ hybridization methods facilitate identification of numerical and structural chromosome abnormalities. We report the development of robust, unique-sequence in situ hybridization probes that have several novel features: 1) they are constructed from multimegabase contigs of yeast artificial chromosome (YAC) clones; 2) they are in the form of adapter-ligated, short-fragment, DNA libraries that may be amplified by polymerase chain reaction; and 3) they have had repetitive sequences (eg, Alu and LINE elements) quant. removed by subtractive hybridization. These subtracted probes are labeled conveniently, and the fluorescence or colorimetric detection signals are extremely bright. Moreover, they constitute a stable resource that may be amplified through at least four rounds of polymerase chain reaction without diminishing signal intensity. We demonstrate applications of subtracted probes for the MYC and EWS oncogene regions, including 1) characterization of a novel EWS-region translocation in Ewing's sarcoma, 2) identification of chromosomal translocations in paraffin sections, and 3) identification of chromosomal translocations by conventional bright-field microscopy.
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 13:55:24 ON 06 AUG 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:55:30 ON 06 AUG 2002

```
L1          384 S LONG (W) (W) (PCR OR POLYMERASE(W)CHAIN)
L2           20 S L1 AND LIGA?
L3           10 DUP REM L2 (10 DUPLICATES REMOVED)
L4           78 S INTRAMOLECULAR (3A) LIGATION
L5            2 S L4 AND HAPLOTYP?
L6           42 DUP REM L4 (36 DUPLICATES REMOVED)
L7          115 S (PCR OR POLYMERASE(W)CHAIN) (11W) (LIGAT? (4A) (AMPLIFIED OR
L8           78 DUP REM L7 (37 DUPLICATES REMOVED)
L9            0 S (PCR OR POLYMERASE(W)CHAIN) (11W) (LIGAT? (4A) (AMPLIFIED OR
L10           2 S (PCR OR POLYMERASE(W)CHAIN) (11W) (LIGAT?)  (15W) REAMPLIF?
L11         104 S (PCR OR POLYMERASE(W)CHAIN) (11W) (LIGAT?)  (15W) AMPLIF?
L12          80 DUP REM L11 (24 DUPLICATES REMOVED)
```

=> d l8 32 bib ab

L8 ANSWER 32 OF 78 MEDLINE DUPLICATE 11
AN 1998267209 MEDLINE
DN 98267209 PubMed ID: 9602151
TI Amplification of target-specific, ligation-dependent circular probe.
AU Zhang D Y; Brandwein M; Hsuih T C; Li H
CS The Lillian, Henry M. Stratton-Hans Popper Department of Pathology, Department of Otolaryngology, Mount Sinai School of Medicine, New York, NY 10029, USA.. david_zhang@smtplink.mssm.edu
SO GENE, (1998 May 12) 211 (2) 277-85.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
EM 199807
ED Entered STN: 19980723
Last Updated on STN: 19980723
Entered Medline: 19980714

AB We describe a novel polymerase chain reaction (PCR)-based gene amplification method utilizing a circularizable oligodeoxyribonucleotide probe (C-probe). The C-probe contains two target complementary regions located at each terminus and an interposed generic PCR primer binding region. The hybridization of C-probe to a target brings two termini in direct apposition as the complementary regions of C-probe wind around the target to form a double helix. Subsequent ligation of the two termini results in a covalently linked C-probe that becomes 'locked on to' the target. The circular nature of the C-probe allows for the generation of a multimeric single-stranded DNA (ssDNA) via extension of the antisense primer by Taq DNA polymerase along the C-probe and displacement of downstream strand, analogous to 'rolling circle' replication of bacteriophage in vivo. This multimeric ssDNA then serves as a template for multiple sense primers to hybridize, extend, and displace downstream DNA, generating a large ramified (branching) DNA complex. Subsequent thermocycling denatures the dsDNA and initiates the next round of primer extension and ramification. This model results in significantly improved amplification kinetics (super-exponential) as compared to conventional PCR. Our results show that the C-probe was 1000 times more sensitive than the corresponding linear hemiprobes for detecting Epstein-Barr virus early RNA. The C-probe not only increases the power of amplification but also offers a means for decontaminating carryover amplicons. As the ligated C-probes possess no free termini, they are resistant to exonuclease digestion, whereas contaminated linear amplicons are susceptible to digestion. Treatment of the ligation reaction mixture with exonuclease prior to amplification eliminated the amplicon contaminant, which could also have been co-amplified with the same **PCR** primers; only the **ligated** C-probes were **amplified**. The combined advantages of the C-probe and thermocycling have a broad applicability for the detection of both DNA and RNA. Finally, we described a novel isothermal amplification method, ramification extension amplification, utilizing circular nature of C-probe and displacement activity of DNA polymerase.

=> d 1-80 ti

L12 ANSWER 1 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Detection and amplification of RNA using target-mediated ligation of DNA by RNA ligase.

L12 ANSWER 2 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Atropisomers of asymmetric xanthene fluorescent dyes and use in DNA sequencing and fragment analysis

L12 ANSWER 3 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Mutant DNA library construction by ligation of overlapping unit DNA fragments and PCR amplification

L12 ANSWER 4 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Haplotyping method for multiple distal nucleotide polymorphisms using long-range PCR

L12 ANSWER 5 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Cyan-green fluorescent protein, GFP variants with stability in a wide pH range created by directed evolution based on site-directed and semi-random mutagenesis

L12 ANSWER 6 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Profiling alternative splicing on fiber-optic arrays.

L12 ANSWER 7 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Highly sensitive ligation-mediated PCR technique demonstrates that multiple clones reconstitute human hematopoiesis in the bone marrow of NOD/SCID mice.

L12 ANSWER 8 OF 80 MEDLINE DUPLICATE 1
TI Blockerette-ligated capture t7-amplified rt-PCR, a new method for determining flanking sequences.

L12 ANSWER 9 OF 80 MEDLINE
TI Novel and alternate SNP and genetic technologies.

L12 ANSWER 10 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Detection and amplification of RNA using target-mediated ligation of DNA by RNA ligase

L12 ANSWER 11 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Multiplex DNA amplification using ligase chain reaction and amplification of ligation products using families of ligatabale probes

L12 ANSWER 12 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Chromosome-wide analysis of protein-DNA interactions

L12 ANSWER 13 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI PCR amplifications of flanking sequences of ORFs in the genome of Synechocystis sp. PCC6803 and a strategy for targeted gene disruption.

L12 ANSWER 14 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Construction of the full-length cDNA of dengue type 2 virus isolated in China.

L12 ANSWER 15 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Breaksite batch mapping, a rapid method for assay and identification of DNA breaksites in mammalian cells

L12 ANSWER 16 OF 80 MEDLINE DUPLICATE 2
TI Highly selective isolation of unknown mutations in diverse DNA fragments: toward new multiplex screening in cancer.

L12 ANSWER 17 OF 80 MEDLINE DUPLICATE 3
TI The ruv proteins of Thermotoga maritima: branch migration and resolution of Holliday junctions.

L12 ANSWER 18 OF 80 MEDLINE DUPLICATE 4
TI Directed evolution of green fluorescent protein by a new versatile PCR strategy for site-directed and semi-random mutagenesis.

L12 ANSWER 19 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI In vitro amplification of circular DNA by a ligation-during amplification method

L12 ANSWER 20 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Nitric oxide-induced damage to mtDNA and its subsequent repair.

L12 ANSWER 21 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI An oligonucleotide-ligation assay for the differentiation between Cyclospora and Eimeria spp. polymerase chain reaction amplification products

L12 ANSWER 22 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Screening of transgenic plants by amplification of unknown genomic DNA flanking T-DNA

L12 ANSWER 23 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Amplification, analysis and chromosome mapping of novel homeobox-containing and homeobox-flanking sequences in rice

L12 ANSWER 24 OF 80 MEDLINE
TI [Microcloning and characteristics of DNA from regions of the centromeric heterochromatin of Drosophila melanogaster polytene chromosomes]. Mikroklonirovanie i kharakteristika DNK iz raionov pritsentromernogo geterokhromatina politennykh khromosom Drosophila melanogaster.

L12 ANSWER 25 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Microcloning and characterization of DNA from pericentromeric heterochromatin of Drosophila melanogaster polytene chromosomes

L12 ANSWER 26 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Selective ligation and amplification method for detection of nucleic acids

L12 ANSWER 27 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Nucleic acid amplification method: hybridization signal amplification method (HSAM)

L12 ANSWER 28 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Method for suppressing DNA fragment amplification during PCR

L12 ANSWER 29 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Method, reagents, and test kit for detecting mutations of causative gene for Werner's syndrome

L12 ANSWER 30 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Two adjacent protein binding motifs in the cbh2 (cellobiohydrolase II-encoding) promoter of the fungus Hypocrea jecorina (Trichoderma reesei) cooperate in the induction by cellulose.

L12 ANSWER 31 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Terminal transferase-dependent PCR: A versatile and sensitive method for in vivo footprinting and detection of DNA adducts.

L12 ANSWER 32 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Subtracted, unique-sequence, in situ hybridization: Experimental and diagnostic applications

L12 ANSWER 33 OF 80 MEDLINE DUPLICATE 5
TI PCR- and ligation-mediated synthesis of marker cassettes with long flanking homology regions for gene disruption in Saccharomyces cerevisiae.

L12 ANSWER 34 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Participation of chromatin in the regulation of phaseolin gene expression.

L12 ANSWER 35 OF 80 MEDLINE DUPLICATE 6
TI Amplification of target-specific, ligation-dependent circular probe.

L12 ANSWER 36 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI The DNA sequence specificity of hedamycin damage determined by ligation-mediated PCR and linear amplification

L12 ANSWER 37 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Transposon display identifies individual transposable elements in high copy number lines.

L12 ANSWER 38 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Application of polymerase chain reaction-oligonucleotide ligation assay for the detection of salmonellae in processed meat, poultry, fish, and pet foods

L12 ANSWER 39 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 7
TI A reliable amplification technique for the characterization of genomic DNA sequences flanking insertion sequences.

L12 ANSWER 40 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Restriction display-PCR of differentially expressed mRNAs using adaptor sequences, cloning into vectors, and kits for determining cell differential gene expression

L12 ANSWER 41 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Ligation-mediated PCR amplification of specific fragments from a Class-II restriction endonuclease

L12 ANSWER 42 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI PCR-amplified cDNA probes for verification of differentially expressed genes

L12 ANSWER 43 OF 80 MEDLINE DUPLICATE 8
TI AFLP markers for DNA fingerprinting in cattle.

L12 ANSWER 44 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI AFLP markers for DNA fingerprinting in cattle.

L12 ANSWER 45 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Movement of Xanthomonas oryzae pv. oryzae in southeast Asia detected using PCR-based DNA fingerprinting.

L12 ANSWER 46 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Shotgun antisense mutagenesis

L12 ANSWER 47 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI In vivo footprinting of the BCL-2 major breakpoint region by ligation-mediated PCR.

L12 ANSWER 48 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Transposon mutagenesis: Cloning of chromosomal DNA from the site of Tn916 insertion using polymerase chain reaction.

L12 ANSWER 49 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI A nucleic acid amplification procedure using a combination of elements from ligase and polymerase chain reactions

L12 ANSWER 50 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Method for suppressing DNA fragment amplification during PCR

L12 ANSWER 51 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Multiplex ligations-dependent amplification using split probe reagents containing common primer binding sites

L12 ANSWER 52 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Rapid screening method of gene amplification products in polypropylene plates

L12 ANSWER 53 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Preparation and use of attenuated RNA virus

L12 ANSWER 54 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Advances in PCR technique applications

L12 ANSWER 55 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Ligation-dependent amplification and non-overlapping oligonucleotide probes for detection of infectious pathogenic microorganisms and abnormal genes

L12 ANSWER 56 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI An assay for detecting nucleic acid sequences combining hybridization, ligation, and PCR amplification of fluorescently labeled primers.

L12 ANSWER 57 OF 80 MEDLINE DUPLICATE 9
TI PCR for direct detection of indigenous uncultured magnetic cocci in sediment and phylogenetic analysis of amplified 16S ribosomal DNA.

L12 ANSWER 58 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI A one-step coupled amplification and oligonucleotide ligation procedure for multiplex genetic typing

L12 ANSWER 59 OF 80 MEDLINE DUPLICATE 10
TI Baboon lipoprotein lipase: cDNA sequence and variable tissue-specific expression of two transcripts.

L12 ANSWER 60 OF 80 MEDLINE DUPLICATE 11
TI Fluorescence-based oligonucleotide ligation assay for analysis of cystic fibrosis transmembrane conductance regulator gene mutations.

L12 ANSWER 61 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI General method for PCR amplification and direct sequencing of mRNA differential display products

L12 ANSWER 62 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Nucleic acid detection methods

L12 ANSWER 63 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Restriction/ligation labeling for primer-initiated amplification of DNA sequences

L12 ANSWER 64 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI In vitro nucleic acid amplification systems

L12 ANSWER 65 OF 80 MEDLINE
TI Competitive titration for probing low-abundance ion channel mRNA molecules in normal and regionally-ischaemic heart tissue.

L12 ANSWER 66 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Single specific primer-polymerase chain reaction (SSP-PCR) and genome walking

L12 ANSWER 67 OF 80 MEDLINE DUPLICATE 12
TI Targeted cloning of a subfamily of LINE-1 elements by subfamily-specific LINE-1-PCR.

L12 ANSWER 68 OF 80 MEDLINE DUPLICATE 13
TI Ligation-anchored PCR: a simple amplification technique with single-sided specificity.

L12 ANSWER 69 OF 80 MEDLINE DUPLICATE 14
TI PCR amplification and analysis of yeast artificial chromosomes.

L12 ANSWER 70 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI PCR amplification of chromosome-specific DNA isolated from flow cytometry-sorted chromosomes

L12 ANSWER 71 OF 80 MEDLINE DUPLICATE 15
TI Cloning and direct sequencing of plant promoters using primer-adapter mediated PCR on DNA coupled to a magnetic solid phase.

L12 ANSWER 72 OF 80 MEDLINE DUPLICATE 16
TI Rapid synthesis of DNA deletion constructs for mRNA quantitation: analysis of astrocyte mRNAs.

L12 ANSWER 73 OF 80 MEDLINE DUPLICATE 17
TI Construction of representative immunoglobulin variable region cDNA libraries from human peripheral blood lymphocytes without in vitro stimulation.

L12 ANSWER 74 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 18
TI LIGATION-MEDIATED PCR APPLICATIONS TO GENOMIC FOOTPRINTING.

L12 ANSWER 75 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI A method and kit for the amplification of unknown nucleotide sequences

L12 ANSWER 76 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI AUTOMATED DNA DIAGNOSTICS USING AN ELISA-BASED OLIGONUCLEOTIDE LIGATION ASSAY.

L12 ANSWER 77 OF 80 MEDLINE DUPLICATE 19
TI Cloning of the shark Po promoter using a genomic walking technique based on the polymerase chain reaction.

L12 ANSWER 78 OF 80 MEDLINE
TI In vivo footprinting of a muscle specific enhancer by ligation mediated PCR.

L12 ANSWER 79 OF 80 MEDLINE DUPLICATE 20
TI Genome walking by single-specific-primer polymerase chain reaction: SSP-PCR.

L12 ANSWER 80 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Ligation-anchored PCR: A simple amplification technique with single-sided specificity.

=> d 79 bib ab

L12 ANSWER 79 OF 80 MEDLINE DUPLICATE 20
AN 90108696 MEDLINE
DN 90108696 PubMed ID: 2691331
TI Genome walking by single-specific-primer polymerase chain reaction: SSP-PCR.
AU Shyamala V; Ames G F
CS Division of Biochemistry and Molecular Biology, University of California, Berkeley 94720.
NC DK12121 (NIDDK)
SO GENE, (1989 Dec 7) 84 (1) 1-8.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals

EM 199002
ED Entered STN: 19900328
Last Updated on STN: 19980206
Entered Medline: 19900213
AB We have devised a strategy to extend the use of the polymerase chain reaction (PCR) to amplify double-stranded DNA when sequence information is available only at one extremity. The only information required is a short stretch of sequence used to design a gene-specific primer, which is then used in combination with a second generic vector primer at the unknown end. The primers are used in a **PCR** reaction after **ligating** the unknown end to a generic vector. Restriction, **ligation, amplification** and sequencing of the products can be achieved within three days. This method eliminates the laborious steps of shotgun cloning, colony screening and culturing of cells. We have used this method to take two contiguous steps beyond the histidine transport operon in Salmonella typhimurium. We also demonstrate the usefulness of this technique to do chromosome walking in the absence of any restriction data.

=> d 75 bib ab

L12 ANSWER 75 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1991:3004 CAPLUS
DN 114:3004
TI A method and kit for the amplification of unknown nucleotide sequences
IN Markham, Alexander Fred; Smith, John Craig; Anwar, Rashida
PA Imperial Chemical Industries PLC, UK
SO Eur. Pat. Appl., 106 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 356021	A2	19900228	EP 1989-307672	19890727
	EP 356021	A3	19911009		
	R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
	ZA 8905473	A	19900328	ZA 1989-5473	19890718
	HU 53944	A2	19901228	HU 1989-3661	19890719
	DK 8903673	A	19900129	DK 1989-3673	19890725
	AU 8938966	A1	19900322	AU 1989-38966	19890725
	AU 635212	B2	19930318		
	NO 8903054	A	19900129	NO 1989-3054	19890726
	FI 8903589	A	19900129	FI 1989-3589	19890727
	GB 2221909	A1	19900221	GB 1989-17143	19890727
	GB 2221909	B2	19921111		
	DD 284053	A5	19901031	DD 1989-331212	19890727
	CN 1040220	A	19900307	CN 1989-107031	19890728
	BR 8903792	A	19900320	BR 1989-3792	19890728
	JP 02174679	A2	19900706	JP 1989-196447	19890728
PRAI	GB 1988-18020		19880728		

AB A method for the amplification of a nucleic acid fragment contg. unknown sequence and kits therefore are provided which enable long nucleotide sequences to be rapidly and efficiently sequenced. The method comprises the formation of target nucleic acid fragment/vectorette units by cleavage of target nucleic acid followed by ligation. One of the nucleic acid fragments will contain an initiating priming region of known sequence for hybridization with an initiating primer and target nucleic acid fragment/vectorette units will contain a vectorette priming region of known sequence for hybridization with a vectorette primer. Amplification is effected by primer extension of an initiating primer hybridized to the

initiating priming region of the target nucleic acid fragment/vectorette unit. DNA of Chlamydia trachomatis serotype L2 was digested with restriction endonuclease EcoRI, vectorette libraries were made using oligonucleotides 27: 5'-AAT TGA AGG AGA GGA CGC TGT CTG TCG AAG GTA AGG AAC GGA GGA GAG AAG GGA GAG-3' and 40: 5'-CTC TCC CTT CTC GAA TCG TAA CCG TTC GTA CGA GAA TCG CTG TCC TCT CCT TC-3', and the target nucleic acid fragment/vectorette was amplified by Taq polymerase using universal vectorette primer 58: CGAATCGTAACCGTTCGTACGAGAATCGCT and primer: 5'-CTGCTCACGTAAATGCACAATTCCG, based on the consensus sequence of MOMP (major outer membrane protein) of Chlamydia L2. The amplified product was purified and sequenced using a universal sequencing primer: 3'-TTCCTCTCCTGTCGC.

=> d 58 bib ab

L12 ANSWER 58 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1995:637903 CAPLUS
DN 123:75795
TI A one-step coupled amplification and oligonucleotide ligation procedure for multiplex genetic typing
AU Eggerding, Faye A.
CS Applied Biosystems Division, Perkin-Elmer Corporation, Foster City, CA, 94404, USA
SO PCR Methods Appl. (1995), 4(6), 337-45
CODEN: PMAPES; ISSN: 1054-9803
DT Journal
LA English
AB A new technique, coupled amplification and oligonucleotide ligation (CAL), has been developed that allows for simultaneous multiplex amplification and genotyping of DNA. CAL is a biphasic method that combines in one assay DNA amplification by PCR with DNA genotyping by the oligonucleotide ligation assay (OLA). By virtue of a difference in the melting temps. of PCR primer-target DNA and OLA probe-target DNA hybrids, the method allows preferential amplification of DNA during stage I and oligonucleotide ligation during stage II of the reaction. In stage I, target DNA is amplified using high-melting primers (Tm values between 68.degree.C and 89.degree.C) in a two-step PCR cycle that employs a 94.degree.C anneal-elongation step. In stage II, genotyping of PCR products by competitive oligonucleotide ligation with oligonucleotide probes (Tm values between 51.degree.C and 67.degree.C) located between the PCR primers is accomplished by several cycles of denaturation at 94.degree.C followed by anneal-ligation at 55.degree.C. Ligation products are fluorochrome-labeled at their 3' ends and analyzed electrophoretically on a fluorescent DNA sequencer. The CAL procedure has been used successfully to analyze human genomic DNA for cystic fibrosis (CF) alleles. Because product detection occurs concurrently with target amplification, the technique is rapid, highly sensitive, and specific and requires minimal sample processing.

=> d 49, 54 56 bib ab

L12 ANSWER 49 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1997:85213 CAPLUS
DN 126:85621
TI A nucleic acid amplification procedure using a combination of elements from ligase and polymerase chain reactions
IN Bhatnagar, Satish K.; George, Albert L., Jr.; Nazarenko, Irina
PA Oncor, Inc., USA
SO PCT Int. Appl., 91 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9639537	A1	19961212	WO 1996-US8841	19960604
	W: AU, BR, CA, CZ, FI, JP, KR, NO, SK, UA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5593840	A	19970114	US 1995-461823	19950605
	AU 9660423	A1	19961224	AU 1996-60423	19960604
PRAI	US 1995-461823		19950605		
	US 1993-10433		19930127		
	US 1993-168621		19931216		
	WO 1996-US8841		19960604		

AB A nucleic acid amplification procedure that uses a combination of ligase and polymerase chain reactions to increase the fidelity of copying of a specific nucleic acid sequence, and to more efficiently detect a particular point mutation in a single assay is described. The amplification products may be exact copies of the template, or may be modified. The basic method uses three primers: two are LCR primers that hybridize adjacent to one another on one strand of the target; the third primer is a complement of the 5' LCR primer and is used to prime polymerase-mediated chain extension. A no. of variations of the method are also described. By cycling through the ligase and **polymerase chain** reactions, the **ligation** product is **amplified**. The ends of primers that are not to be used as substrates may be modified, e.g. by use of a 3'-arabinosyl nucleotide at the end of a the 3' LCR primer or the use of phosphorothioate groups to inhibit nucleases. The method can be used with single- and double-stranded nucleic acid substrates.

L12 ANSWER 54 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1997:448753 CAPLUS
DN 127:157230
TI Advances in PCR technique applications
AU Zhang, Hongying; Zhang, Jin
CS State Key Laboratory Enzyme Engineering, Jilin University, Changchun, 130023, Peop. Rep. China
SO Shengwu Huaxue Yu Shengwu Wuli Jinzhan (1996), 23(6), 509-513
CODEN: SHYCD4; ISSN: 1000-3282
PB Kexue
DT Journal; General Review
LA Chinese
AB A review with 18 refs. on **PCR** technique applications including **ligation**-independent cloning, random-primed/anchored PCR, random rapid **amplification** of cDNA ends, recombinant PCR and megaprimer PCR.

L12 ANSWER 56 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1995:522764 CAPLUS
DN 122:257956
TI An assay for detecting nucleic acid sequences combining hybridization, ligation, and PCR amplification of fluorescently labeled primers.
IN Yamagata, Koichi; Umemura, Isao; Shibatani, Takeji
PA Tanabe Seiyaku Co., Ltd., Japan; Eiken Chemical Co., Ltd.
SO Eur. Pat. Appl., 12 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI	EP 639647	A2	19950222	EP 1994-110526	19940706
	R: DE, FR, GB, IT				
	JP 07023800	A2	19950127	JP 1993-168895	19930708
PRAI	JP 1993-168895		19930708		

AB An assay for detecting nucleic acid sequences is presented. The first steps comprise contacting (1) a target single-stranded nucleic acid, (2) a pair of nucleic acid primers having nucleotide sequence complementary to the target nucleic acid and its complementary chain, resp., (3) a fluorescently-labeled nucleic acid probe which has a nucleotide sequence designed to be hybridized to the target nucleic acid downstream (at the side of 3'-terminus) from where the nucleic acid primer is hybridized and has a modified 3'-end so that the nucleotide chain is not elongated by a nucleic acid polymerase, and (4) a nucleic acid polymerase having exonuclease activity specific to a double-stranded nucleic acid in the presence of substrates for the enzyme (4 kinds of nucleoside triphosphate), and thereby elongating the said nucleic acid primer chain and simultaneously hydrolyzing only the fluorescently-labeled nucleic acid probe hybridized to the target nucleic acid. The chain-elongated product of primer is denatured to a single-stranded form. Amplification of the target nucleic acid is achieved by repeating the above steps, and the change in fluorescence polarization resulted from hydrolysis of the probe is detd. This method is effective for detection of target nucleic acid sequences more simply and with higher sensitivity and higher reliability in comparison with known methods. Further, it has advantages that because of no carryover or contamination of the amplified nucleic acids into subsequent reactions, undesirable false pos. result can be avoided. The method is illustrated for the detection of M13mp18 phage DNA as the target, fluorescein isocyanate as the fluorescent label, and Taq DNA polymerase as the nucleic acid polymerase with double-strand exonuclease activity.

=> d 26, 27, 33, 39 bib ab

L12 ANSWER 26 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1998:605032 CAPLUS
DN 129:198865
TI Selective ligation and amplification method for detection of nucleic acids
IN Todd, Alison Velyian; Fuery, Caroline Jane
PA Johnson & Johnson Research Pty. Ltd., Australia
SO PCT Int. Appl., 31 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9837230	A1	19980827	WO 1998-AU114	19980223
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9859762	A1	19980909	AU 1998-59762	19980223
	AU 728342	B2	20010104		
	EP 1002124	A1	20000524	EP 1998-902877	19980223
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

	BR 9807253	A	20010828	BR 1998-7253	19980223
	JP 2001517936	T2	20011009	JP 1998-536095	19980223
	US 6245505	B1	20010612	US 1999-367825	19991217
PRAI	AU 1997-5248	A	19970221		
	WO 1998-AU114	W	19980223		

AB The present invention provides a method for amplifying a specific target nucleic acid sequence using both LCR and PCR. This method is called SLAP (Selective Ligation and PCR). The method comprises (1) forming a reaction mixt. comprising: (a) the target sequence; (b) primers comprising a first primer at least a portion of which at the 3' end thereof is substantially complementary to a first segment at a first end of the target sequence, a second primer at least a portion of which at the 5' end thereof is substantially complementary to a second segment at a second end of the target sequence, the 5' end of the second primer being adjacent the 3' end of the first primer, and a third primer, the third primer being substantially complementary to a segment of the second primer at the 3' end thereof; (c) at least four different nucleotide bases; (d) thermostable polymerase and thermostable ligase; and (2) thermocycling the reaction mixt. The SLAP method was used to detect point mutations of the K-ras oncogene.

L12 ANSWER 27 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 1998:106058 CAPLUS
DN 128:176931
TI Nucleic acid amplification method: hybridization signal amplification method (HSAM)
IN Zhang, David Y.; Brandwein, Margaret
PA Mount Sinai School of Medicine of the City University of New York, USA
SO PCT Int. Appl., 137 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 5

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9804745	A1	19980205	WO 1997-US13390	19970730
	W: JP				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5876924	A	19990302	US 1996-690495	19960731
	EP 1007728	A1	20000614	EP 1997-935207	19970730
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2001521373	T2	20011106	JP 1998-509121	19970730
PRAI	US 1996-690495	A	19960731		
	US 1994-263937	B2	19940622		
	US 1996-596331	A2	19960520		
	WO 1997-US13390	W	19970730		

AB An improved method allowing for rapid sensitive and standardized detection of a target nucleic acid from a pathogenic microorganism or virus or normal or abnormal gene in a sample is provided. The method involves hybridizing a target nucleic acid to several non-overlapping oligonucleotide probes that hybridize to adjacent regions in the target nucleic acid, the probes being referred to as capture/amplification probes and amplification probes, resp., in the presence of paramagnetic beads coated with a ligand binding moiety. Through the binding of a ligand attached to one end of the capture/amplification probe and the specific hybridization of portions of the probes to adjacent sequences in the target nucleic acid, a complex comprising the target nucleic acid, the probes and the paramagnetic beads is formed. The probes may then be ligated together to form a contiguous ligated amplification sequence bound to the beads, which complex may be denatured to remove the target nucleic acid and unligated probes. Alternatively, sep. capture and amplification

probes may be used which form continuous full-length or circular probes, and may be directly detected or amplified using a suitable amplification technique, e.g., PCR, RAM or HSAM for detection. The detection of the ligated amplification sequence, either directly or following amplification of the ligated amplification sequence, indicates the presence of the target nucleic acid in a sample. Methods for the detection of the ligated amplification sequence, including hybridization signal amplification method and ramification-extension amplification method, are also provided. HSAM is demonstrated for the detection of (1) the gag gene of HIV-1 RNA in a sample, (2) 16S rRNA of Mycobacterium avium/intracellulare, (3) hepatitis C virus RNA in a sample, and (4) Epstein-Barr virus RNA (EBER-1) in parotid pleomorphic adenomas.

L12 ANSWER 33 OF 80 MEDLINE DUPLICATE 5
AN 1998108026 MEDLINE
DN 98108026 PubMed ID: 9443982
TI PCR- and ligation-mediated synthesis of marker cassettes with long flanking homology regions for gene disruption in Saccharomyces cerevisiae.
AU Nikawa J; Kawabata M
CS Department of Biochemical Engineering and Science, Faculty of Computer Science and Systems Engineering, Kyushu Institute of Technology, Iizuka, Fukuoka 820, Japan.. nikawa@bse.kyutech.ac.jp
SO NUCLEIC ACIDS RESEARCH, (1998 Feb 1) 26 (3) 860-1.
Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199803
ED Entered STN: 19980319
Last Updated on STN: 19980319
Entered Medline: 19980312
AB We developed a novel method for synthesizing marker-disrupted alleles of yeast genes. The first step is PCR amplification of two sequences located upstream and downstream of the reading frame to be disrupted. Due to the addition of non-specific single A overhangs by Taq DNA polymerase, each **PCR** product can be **ligated** with a marker DNA which has T residues at its 3' ends. After **amplification** of individual ligation products through the second PCR, both products are mixed and annealed, and the single strand is converted to a double strand by an extension reaction. The final step is PCR amplification of the fragment composed of a selectable marker and two flanking sequences with the outermost primers. This method is rapid and needs only short oligonucleotides as primers.

L12 ANSWER 39 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 7
AN 1998:93208 BIOSIS
DN PREV199800093208
TI A reliable amplification technique for the characterization of genomic DNA sequences flanking insertion sequences.
AU Prod'hom, Guy; Lagier, Beatrice; Pelicic, Vladimir; Hance, Allan J.; Gicquel, Brigitte; Guilhot, Christophe (1)
CS (1) Unite Genetique Mycobacterienne, Inst. Pasteur, 25 rue du Dr. Roux, 75724 Paris Cedex 15 France
SO FEMS Microbiology Letters, (Jan. 1, 1998) Vol. 158, No. 1, pp. 75-81.
ISSN: 0378-1097.
DT Article
LA English
AB A simple and efficient ligation-mediated PCR (LMPCR) is described for amplifying DNA adjacent to known sequences. The method uses one primer specific for the known sequence and a second specific for a synthetic

linker ligated to restricted genomic DNA. Perkin-Elmer AmpliTaq Gold polymerase is used to minimize non-specific primer annealing and amplification. This LMPCR method was successfully applied to isolate DNA sequences flanking mobile elements present in mycobacterial mutants generated by transposon mutagenesis.

=> FIL STNGUIDE

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-6.20	-6.20

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LAST RELOADED: Aug 2, 2002 (20020802/UP).

=> d 4 bib ab
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L12 ANSWER 4 OF 80 CAPLUS COPYRIGHT 2002 ACS
AN 2002:488130 CAPLUS
DN 137:58558
TI Haplotyping method for multiple distal nucleotide polymorphisms using long-range PCR
IN Evans, William Edward; McDonald, Oliver Gene
PA USA
SO U.S. Pat. Appl. Publ., 11 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2002081598	A1	20020627	US 2001-829113	20010409

AB The invention relates to methods for detecting genetic polymorphisms in an organism, particularly to the detection of genetic polymorphisms that are due to multiple distal nucleotide polymorphisms within a gene. Methods are provided for detg. the haplotype structure of a gene, or other contiguous DNA segment, having two or more nucleotide polymorphisms that are sepd. by kilobases of DNA. The methods involve the use of PCR amplification and DNA ligation to bring the nucleotide polymorphisms on a particular allele of the gene into close proximity to facilitate the detn. of haplotype structure. The method is exemplified by genotyping human thiopurine S-methyltransferase (TPMT) gene for two SNPs (G460A and A719G) sepd. by approx. 8 kb. A long-range PCR reaction is performed by two PCR reactions. The first PCR uses a DNA sample contg. the TPMT gene and a first set of oligonucleotide primers designed for the amplification of the two SNPs and the region of the TPMT gene sepg. them. The resulting approx. 8.7 kb **PCR** product is then circularized via intramol. **ligation**, and is subjected to a second PCR **amplification** using a second pair of oligonucleotide primers lying adjacent to the circular DNA. The second PCR product is approx. 1.2 kb and comprises both

SNPs sepd. by 695 nucleotides. The haplotype structure of the second PCR product can then be detd. by std. methods for SNPs that are sepd. by less than about 1 kilobase.